

Query Match 60.3%; Score 622; DB 2; Length 204;
Best Local Similarity 58.5%; Pred. No. 3.6e-45;
Matches 117; Conservative 35; Mismatches 48; Indels 0; Gaps 0;

Qy 1
MFKFLKRVVFLAFLIFCFYQAYITHQNVQNMQYKPMVEKTLAENDTTANVNL
VLAMIYT 60

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Db 1
MFKRIRRVLVLAFLFAGYKAYRVHQDVKQVMTYQPMVREILSEQDTPANEEL
VLAMIYT 60

Qy 61
ETKGGQADVMQSSSESSGVTNSITDSQSSIQHGVKLLSENLTAEKAGVDSWTA
VQAYNF 120

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Db 61
ETKGKEGDVMQSSSESAGSTNTINDNASSIRQGIQTLTGNNLYLAQKKGVDIWTAV
QAYNF 120

Qy 121
GTAYIDYVAKNGGDNTISLASHYSKSVVAPSLGNKDGKMYLYYHPIALLYGGKL
YQNGGN 180

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Db 121
GPAYIDFIAQNGKENTLALAKQYSRETVAPLLGNRTGKTYSYIHPISIFHGAELYV
NGGN 180

Qy 181 IYYSREVHFNYYLIQLLSKF 200

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Db 181 YYYSRQVRLNLYIIKCFTLF 200